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1996

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SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<121> POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT, K-betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE

<130> D0121 NP

<150> US 60/270,132

<151> 2001-02-21

<150> US 60/278,953

<151> 2001-03-27

<160> 74

<170> PatentIn version 3.0

<210> 1

<211> 2052

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (121)..(1095)

<400> 1

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tgcagctcct gagtgcagcg cggcttctctg ccactgtccc ggcccggcca cctctctgtc      120

atg gct ctg gcg gac agc aca cgt gga tta ccc aac ggg ggc ggc ggc      168
Met Ala Leu Ala Asp Ser Thr Arg Gly Leu Pro Asn Gly Gly Gly Gly
1          5          10          15

ggg ggc ggc agt ggc tcc tcg tcg tcc tcc gcg gag cca ccg ctc ttc      216
Gly Gly Gly Ser Gly Ser Ser Ser Ser Ser Ala Glu Pro Pro Leu Phe
20          25          30

ccc gac atc gtg gag ctg aac gtg ggg ggc cag gtg tac gtg acc cgg      264
Pro Asp Ile Val Glu Leu Asn Val Gly Gly Gln Val Tyr Val Thr Arg
35          40          45

cgc tgc acg gtg gtg tcg gtg ccc gac tcg ctg ctc tgg cgc atg ttc      312
Arg Cys Thr Val Val Ser Val Pro Asp Ser Leu Leu Trp Arg Met Phe
50          55          60

acg cag cag cag ccg cag gag ctg gcc cgg gac agc aaa ggc cgc ttc      360
Thr Gln Gln Gln Pro Gln Glu Leu Ala Arg Asp Ser Lys Gly Arg Phe
65          70          75          80

ttt ctg gac cgg gac ggc ttc ctc ttc cgc tac atc ctg gat tac ctg      408
Phe Leu Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu
85          90          95

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egg gac ttg cag ctc gtg ctg ccc gac tac ttc ccc gag cgc agc egg	456
Arg Asp Leu Gln Leu Val Leu Pro Asp Tyr Phe Pro Glu Arg Ser Arg	
100 105 110	
ctg cag cgc gag gcc gag tac ttc gag ctg cca gag ctc gtg cgc cgc	504
Leu Gln Arg Glu Ala Glu Tyr Phe Glu Leu Pro Glu Leu Val Arg Arg	
115 120 125	
ctc ggg gcc ccc cag cag ccc gcc ccg ggg ccg ccg ccc tcg cgg cgc	552
Leu Gly Ala Pro Gln Gln Pro Gly Pro Gly Pro Pro Pro Ser Arg Arg	
130 135 140	
ggg gtg cac aag gag gcc tcg ctg ggt gac gag ctg ctg ccg ctt gcc	600
Gly Val His Lys Glu Ser Leu Gly Asp Glu Leu Leu Pro Leu Gly	
145 150 155 160	
tac tcg gag ccc gaa cag cag gag gcc gcc tct gcc ggg gcg ccg tcg	648
Tyr Ser Glu Pro Glu Gln Gln Glu Gly Ala Ser Ala Gly Ala Pro Ser	
165 170 175	
ccc acg ctg gag ctg gct agc cgc agt ccg tcc ggg gcc gcg gcg gcc	696
Pro Thr Leu Glu Leu Ala Ser Arg Ser Pro Ser Gly Gly Ala Ala Gly	
180 185 190	
ccg ctg ctc acg ccg tcc cag tcg ctg gac gcc agc ccg cgc tcg gcc	744
Pro Leu Leu Thr Pro Ser Gln Ser Leu Asp Gly Ser Arg Arg Ser Gly	
195 200 205	
tac atc acc atc gcc tac cgc gcc tcc tac acc atc ggg ccg gac gcg	792
Tyr Ile Thr Ile Gly Tyr Arg Gly Ser Tyr Thr Ile Gly Arg Asp Ala	
210 215 220	
cag gcg gac gcc aag ttc cgg cga gtg gcg cgc atc acc gtt tgc gga	840
Gln Ala Asp Ala Lys Phe Arg Arg Val Ala Arg Ile Thr Val Cys Gly	
225 230 235 240	
aag acg tcg ctg gcc aag gag gtg ttt ggg gac acc ctg aac gaa agc	888
Lys Thr Ser Leu Ala Lys Glu Val Phe Gly Asp Thr Leu Asn Glu Ser	
245 250 255	
cgg gac ccc gac cgt ccc ccg gag cgc tac acc tcg cgc tat tac ctc	936
Arg Asp Pro Asp Arg Pro Pro Glu Arg Tyr Thr Ser Arg Tyr Tyr Leu	
260 265 270	
aag ttc aac ttc ctg gag cag gcc ttc gac aag ctg tcc gag tcg gcc	984
Lys Phe Asn Phe Leu Glu Gln Ala Phe Asp Lys Leu Ser Glu Ser Gly	
275 280 285	
ttc cac atg gtg gcg tgc agc tcc acg gcc acc tgc gcc ttt gcc agc	1032
Phe His Met Val Ala Cys Ser Ser Thr Gly Thr Cys Ala Phe Ala Ser	
290 295 300	
agc acc gac cag agc gag gac aag atc tgg acc agc tac acc gag tac	1080
Ser Thr Asp Gln Ser Glu Asp Lys Ile Trp Thr Ser Tyr Thr Glu Tyr	
305 310 315 320	
gtc ttc tgc agg gag tgagctcccc agacccccc gccactccag cgcgccagtc	1135

Val Phe Cys Arg Glu
325

ttctcctgccc	cgagagatga	ttacagagccc	tcttggtccca	cctttgtccc	ctgggtgctg	1195
ccctccatt	ctcccccctcc	agtagtagct	gggtgagacc	tgccgccc	ccttccctcc	1255
actacagaac	ctggagccgc	aaatcctctg	ggctgcttcg	tcttctttgg	acctcctgaa	1315
cagagagaac	ccagaggaac	ccccacccc	ccccaccta	ccactccatg	ctttctctac	1375
tccctgctc	aaaccacccc	tccccagat	ggtacttcag	tttggatcta	ttgggggagt	1435
gtggccacag	acggggggat	gattgaattg	ttcagaacct	gattggaccg	tgccaatgt	1495
ggggaagatt	tcttgaaaat	cttctcaage	tcttatgact	cactgggggt	ttaagagato	1555
aggattgggt	ccactgtctg	gggttagtgt	tttacaaggt	cattacacag	tctttttgac	1615
ctcttttgaa	ggtagagttt	tagaaggctg	gatggaagat	tctgagcctg	gaattaggac	1675
cccatggagg	cagtcctcaa	accaccctc	ccccagatgg	tacttcagtt	tggtctatt	1735
gggggagtgt	ggccacagac	cgggggatga	ttgaattgtt	cagaacctga	ttggaccgtg	1795
tccaatgtgc	ggaagatttc	cttgaaatct	tctcaagctc	ttatgactca	ctgggggttt	1855
aagagatcag	gattggttcc	actgtctggg	gttagtgttt	tacaaggcca	ttacacagtc	1915
tttttgacct	cttttgaagg	tagagtttta	gaaggctgga	tggaagattc	tgagcctgga	1975
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<211> 325
<212> PRT
<213> homo sapiens

<400> 2

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Gly	Gly	Gly	Ser	Gly	Ser	Ser	Ser	Ser	Ser	Ala	Glu	Pro	Pro	Leu	Phe
			20					25					30		

Pro	Asp	Ile	Val	Glu	Leu	Asn	Val	Gly	Gly	Gln	Val	Tyr	Val	Thr	Arg
		35					40					45			

Arg	Cys	Thr	Val	Val	Ser	Val	Pro	Asp	Ser	Leu	Leu	Trp	Arg	Met	Phe
	50					55					60				

Thr Gln Gln Gln Pro Gln Glu Leu Ala Arg Asp Ser Lys Gly Arg Phe
65 70 75 80

Phe Leu Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu
85 90 95

Arg Asp Leu Gln Leu Val Leu Pro Asp Tyr Phe Pro Glu Arg Ser Arg
100 105 110

Leu Gln Arg Glu Ala Glu Tyr Phe Glu Leu Pro Glu Leu Val Arg Arg
115 120 125

Leu Gly Ala Pro Gln Gln Pro Gly Pro Gly Pro Pro Pro Ser Arg Arg
130 135 140

Gly Val His Lys Glu Gly Ser Leu Gly Asp Glu Leu Leu Pro Leu Gly
145 150 155 160

Tyr Ser Glu Pro Glu Gln Gln Glu Gly Ala Ser Ala Gly Ala Pro Ser
165 170 175

Pro Thr Leu Glu Leu Ala Ser Arg Ser Pro Ser Gly Gly Ala Ala Gly
180 185 190

Pro Leu Leu Thr Pro Ser Gln Ser Leu Asp Gly Ser Arg Arg Ser Gly
195 200 205

Tyr Ile Thr Ile Gly Tyr Arg Gly Ser Tyr Thr Ile Gly Arg Asp Ala
210 215 220

Gln Ala Asp Ala Lys Phe Arg Arg Val Ala Arg Ile Thr Val Cys Gly
225 230 235 240

Lys Thr Ser Leu Ala Lys Glu Val Phe Gly Asp Thr Leu Asn Glu Ser
245 250 255

Arg Asp Pro Asp Arg Pro Pro Glu Arg Tyr Thr Ser Arg Tyr Tyr Leu
260 265 270

Lys Phe Asn Phe Leu Glu Gln Ala Phe Asp Lys Leu Ser Glu Ser Gly
275 280 285

Phe His Met Val Ala Cys Ser Ser Thr Gly Thr Cys Ala Phe Ala Ser
 290 295 300

Ser Thr Asp Gln Ser Glu Asp Lys Ile Trp Thr Ser Tyr Thr Glu Tyr
 305 310 315 320

Val Phe Cys Arg Glu
 325

<210> 3
 <211> 228
 <212> PRT
 <213> Drosophila melanogaster

<400> 3

Met Pro Glu Ile Ile Glu Leu Asn Val Gly Gly Val Ser Tyr Thr Thr
 1 5 10 15

Thr Leu Ala Thr Leu Leu Gln Asp Lys Ser Thr Leu Leu Ala Glu Leu
 20 25 30

Phe Gly Glu Gly Arg Asp Ser Leu Ala Lys Asp Ser Lys Gly Arg Tyr
 35 40 45

Phe Leu Asp Arg Asp Gly Val Leu Phe Arg Tyr Ile Leu Asp Phe Leu
 50 55 60

Arg Asp Lys Ala Leu His Leu Pro Glu Gly Phe Arg Glu Arg Gln Arg
 65 70 75 80

Leu Leu Arg Glu Ala Glu His Phe Lys Leu Thr Ala Met Leu Glu Cys
 85 90 95

Ile Arg Ser Glu Arg Asp Ala Arg Pro Pro Gly Cys Ile Thr Ile Gly
 100 105 110

Tyr Arg Gly Ser Phe Gln Phe Gly Lys Asp Gly Leu Ala Asp Val Lys
 115 120 125

Phe Arg Lys Leu Ser Arg Ile Leu Val Cys Gly Arg Val Ala Gln Cys
 130 135 140

Arg Glu Val Phe Gly Asp Thr Leu Asn Glu Ser Arg Asp Pro Asp His
 145 150 155 160

Gly Gly Thr Asp Arg Tyr Thr Ser Arg Phe Phe Leu Lys His Cys Tyr
 165 170 175

Ile Glu Gln Ala Phe Asp Asn Leu His Asp His Gly Tyr Arg Met Ala
 180 185 190

Gly Ser Cys Gly Ser Gly Thr Ala Gly Ser Ala Ala Glu Pro Lys Pro

195

200

205

Gly Val Asp Thr Glu Glu Asn Arg Trp Asn His Tyr Asn Glu Phe Val
 210 215 220

Phe Ile Arg Asp
 225

<210> 4
 <211> 435
 <212> PRT
 <213> Homo sapiens

<400> 4

Gln Gln Gln Lys Lys Gly Thr Met Ala Leu Ser Gly Asn Cys Ser Arg
 1 5 10 15

Tyr Tyr Pro Arg Glu Gln Gly Ser Ala Val Pro Asn Ser Phe Pro Glu
 20 25 30

Val Val Glu Leu Asn Val Gly Gly Gln Val Tyr Phe Thr Arg His Ser
 35 40 45

Thr Leu Ile Ser Ile Pro His Ser Leu Leu Trp Lys Met Phe Ser Pro
 50 55 60

Lys Arg Asp Thr Ala Asn Asp Leu Ala Lys Asp Ser Lys Gly Arg Phe
 65 70 75 80

Phe Ile Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu
 85 90 95

Arg Asp Arg Gln Val Val Leu Pro Asp His Phe Pro Glu Lys Gly Arg
 100 105 110

Leu Lys Arg Glu Ala Glu Tyr Phe Gln Leu Pro Asp Leu Val Lys Leu
 115 120 125

Leu Thr Pro Asp Glu Ile Lys Gln Ser Pro Asp Glu Phe Cys His Ser
 130 135 140

Asp Phe Glu Asp Ala Ser Gln Gly Ser Asp Thr Arg Ile Cys Pro Pro
 145 150 155 160

Ser Ser Leu Leu Pro Ala Asp Arg Lys Trp Gly Phe Ile Thr Val Gly
 165 170 175

Tyr Arg Gly Ser Cys Thr Leu Gly Arg Glu Gly Gln Ala Asp Ala Lys
 180 185 190

Phe Arg Arg Val Pro Arg Ile Leu Val Cys Gly Arg Ile Ser Leu Ala
 195 200 205

Lys Glu Val Phe Gly Glu Thr Leu Asn Glu Ser Arg Asp Pro Asp Arg
 210 215 220

Ala Pro Glu Arg Tyr Thr Ser Arg Phe Tyr Leu Lys Phe Lys His Leu
225 230 235 240

Glu Arg Ala Phe Asp Met Leu Ser Glu Cys Gly Phe His Met Val Ala
245 250 255

Cys Asn Ser Ser Val Thr Ala Ser Phe Ile Asn Gln Tyr Thr Asp Asp
260 265 270

Lys Ile Trp Ser Ser Tyr Thr Glu Tyr Val Phe Tyr Arg Glu Pro Ser
275 280 285

Arg Trp Ser Pro Ser His Cys Asp Cys Cys Cys Lys Asn Gly Lys Gly
290 295 300

Asp Lys Glu Gly Glu Ser Gly Thr Ser Cys Asn Asp Leu Ser Thr Ser
305 310 315 320

Ser Cys Asp Ser Gln Ser Glu Ala Ser Ser Pro Gln Glu Thr Val Ile
325 330 335

Cys Gly Pro Val Thr Arg Gln Thr Asn Ile Gln Thr Leu Asp Arg Pro
340 345 350

Ile Lys Lys Gly Pro Val Gln Leu Ile Gln Gln Ser Glu Met Arg Arg
355 360 365

Lys Ser Asp Leu Leu Arg Thr Leu Thr Ser Gly Ser Arg Glu Ser Asn
370 375 380

Met Ser Ser Lys Lys Lys Ala Val Lys Glu Lys Leu Ser Ile Glu Glu
385 390 395 400

Glu Leu Glu Lys Cys Ile Gln Asp Phe Leu Lys Ile Lys Ile Pro Asp
405 410 415

Arg Phe Pro Glu Arg Lys His Pro Trp Gln Ser Glu Leu Leu Arg Lys
420 425 430

Tyr His Leu
435

<210> 5
<211> 140
<212> PRT
<213> Caenorhabditis elegans

<400> 5

Met Thr Ser Val Glu Asp Val Ile Thr Leu Asn Val Gly Gly Thr Met
1 5 10 15

Tyr Thr Thr Thr Arg Ser Thr Leu Ser Lys Glu Thr Asp Thr Leu Leu
20 25 30

Ala Asn Ile Ala Ser Gly Ser Leu Ser Glu Asp Glu Gln Ala Asn Val
35 40 45

Val Thr Leu Pro Asp Gly Thr Leu Phe Val Asp Arg Asp Gly Pro Leu
 50 55 60
 Phe Ala Tyr Val Leu His Phe Leu Arg Thr Asp Lys Leu Ser Leu Pro
 65 70 75 80
 Glu Gln Phe Arg Glu Val Ala Arg Leu Lys Asp Glu Ala Asp Phe Tyr
 85 90 95
 Arg Leu Glu Arg Phe Ser Thr Leu Leu Ser Asn Ala Ser Ser Ile Ser
 100 105 110
 Pro Arg Pro Arg Thr Ala Asn Gly Tyr Asn Thr Ile Thr Ser Gly Ala
 115 120 125
 Glu Thr Gly Gly Tyr Ile Thr Leu Gly Tyr Arg Gly
 130 135 140

<210> 6
 <211> 256
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> UNSURE
 <222> (15)..(15)
 <223> wherein "X" is equal to any amino acid.

<400> 6

Met Ser Arg Pro Leu Ile Thr Arg Ser Pro Ala Ser Pro Leu Xaa Asn
 1 5 10 15
 Gln Gly Ile Pro Thr Pro Ala Gln Leu Thr Lys Ser Asn Ala Pro Val
 20 25 30
 His Ile Asp Val Gly Gly His Met Tyr Thr Ser Ser Leu Ala Thr Leu
 35 40 45
 Thr Lys Tyr Pro Glu Ser Arg Ile Gly Arg Leu Phe Asp Gly Thr Glu
 50 55 60
 Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp
 65 70 75 80
 Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu
 85 90 95
 Leu Ile Pro Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala
 100 105 110
 Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys
 115 120 125
 Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val

130	135	140
Val Arg Val Ala Pro Asp Leu Gly Glu Arg Ile Thr Leu Ser Gly Asp		
145	150	155 160
Lys Ser Leu Ile Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys		
	165 170	175
Asn Ser Val Asn Ala Gly Trp Asn His Asp Ser Thr His Val Ile Arg		
	180 185	190
Phe Pro Leu Asn Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu		
	195 200	205
Arg Leu Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Gly Gly Gly		
	210 215	220
Val Asp Ser Ser Gln Phe Ser Glu Tyr Val Leu Arg Arg Glu Leu Arg		
	225 230	235 240
Arg Thr Pro Arg Val Pro Ser Val Ile Arg Ile Lys Gln Glu Pro Leu		
	245 250	255

<210> 7
 <211> 237
 <212> PRT
 <213> Homo sapiens

<400> 7

Met Asp Asn Gly Asp Trp Gly Tyr Met Met Thr Asp Pro Val Thr Leu	
1	5 10 15
Asn Val Gly Gly His Leu Tyr Thr Thr Ser Leu Thr Thr Leu Thr Arg	
	20 25 30
Tyr Pro Asp Ser Met Leu Gly Ala Met Phe Gly Gly Asp Phe Pro Thr	
	35 40 45
Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu	
	50 55 60
Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro	
	65 70 75 80
Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr	
	85 90 95
Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr	
	100 105 110
Pro Met Asp Thr Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys	
	115 120 125
Leu Ser Lys Tyr Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr	
	130 135 140

Ile Thr Thr Lys Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe
145 150 155 160

Thr Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser
165 170 175

Phe Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val
180 185 190

His Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr
195 200 205

Arg Val His His Met Ser Glu Arg Ala Asn Glu Asn Thr Val Glu His
210 215 220

Asn Trp Thr Phe Cys Arg Leu Ala Arg Lys Thr Asp Asp
225 230 235

<210> 8
<211> 688
<212> DNA
<213> homo sapiens

<220>
<221> misc_feature
<223> wherein "N" is equal to "A", "C", "G" or "T".

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gagtgcagcg cggttctctg ccaactgtccc ggcccggcca cctctctgtc atggctctgg 120
cggacagcac acgtggatta cccaannnnn nnnnnnnnnn nnnnnnnnagt ggctcctcgt 180
cgtcctccgc ggagccaccg ctcttccccc acatcgtgga gctgaacgtg gggggccagg 240
tgtacgtgac ccggcgctgc acggtgggtgt cggtgccga ctcgctgctc tggcgcatgt 300
tcacgcagca gcagccgcag gagctggccc gggacagcaa aggccgcttc tttctggacc 360
gggaacgggtt cctcttccgc tacatcctgg attacctgcg ggacttgcag ctcgctgctg 420
ccgactactt ccccgagcgc agccggctgc agcgcgaggc cgagtacttc gagctgccag 480
agctcgtnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 540
nnnnntgca caaggagggc tcgctgggtg acgagctgct gccgcttggc tactcggagc 600
ccgaacagca ggagggcgcc tctgccgggg cgcgctgcc cacgctggag ctggctagcc 660
gcagtcgtn nnnnnnnnnn nnnnnnnn 688

<210> 9
<211> 237
<212> PRT

<213> homo sapiens

<400> 9

Met Asp Asn Gly Asp Trp Gly Tyr Met Met Thr Asp Pro Val Thr Leu
1 5 10 15

Asn Val Gly Gly His Leu Tyr Thr Thr Ser Leu Thr Thr Leu Thr Arg
20 25 30

Tyr Pro Asp Ser Met Leu Gly Ala Met Phe Gly Gly Asp Phe Pro Thr
35 40 45

Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu
50 55 60

Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro
65 70 75 80

Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr
85 90 95

Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr
100 105 110

Pro Met Asp Thr Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys
115 120 125

Leu Ser Lys Tyr Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr
130 135 140

Ile Thr Thr Lys Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe
145 150 155 160

Thr Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser
165 170 175

Phe Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val
180 185 190

His Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr
195 200 205

Arg Val His His Met Ser Glu Arg Ala Asn Glu Asn Thr Val Glu His
210 215 220

Asn Trp Thr Phe Cys Arg Leu Ala Arg Lys Thr Asp Asp
225 230 235

<210> 10

<211> 80

<212> DNA

<213> homo sapiens

<400> 10

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aggatgttagc ggaagaggaa

50

<210> 11
<211> 19
<212> DNA
<213> homo sapiens

<400> 11
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19

<210> 12
<211> 20
<212> DNA
<213> homo sapiens

<400> 12
agctctggca gctcgaagta

20

<210> 13
<211> 101
<212> PRT
<213> homo sapiens

<400> 13

Asp Ile Val Glu Leu Asn Val Gly Gly Gln Val Tyr Val Thr Arg Arg
1 5 10 15

Cys Thr Val Val Ser Val Pro Asp Ser Leu Leu Trp Arg Met Phe Thr
20 25 30

Gln Gln Gln Pro Gln Glu Leu Ala Arg Asp Ser Lys Gly Arg Phe Phe
35 40 45

Leu Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu Arg
50 55 60

Asp Leu Gln Leu Val Leu Pro Asp Tyr Phe Pro Glu Arg Ser Arg Leu
65 70 75 80

Gln Arg Glu Ala Glu Tyr Phe Glu Leu Pro Glu Leu Val Arg Arg Leu
85 90 95

Gly Ala Pro Gln Gln
100

<210> 14
<211> 13
<212> PRT
<213> homo sapiens

<400> 14

Met Ala Leu Ala Asp Ser Thr Arg Gly Leu Pro Asn Gly

1 5 10

<210> 15
<211> 13
<212> PRT
<213> homo sapiens

<400> 15

Gly Gln Val Tyr Val Thr Arg Arg Cys Thr Val Val Ser
1 5 10

<210> 16
<211> 13
<212> PRT
<213> homo sapiens

<400> 16

Pro Gly Pro Pro Pro Ser Arg Arg Gly Val His Lys Glu
1 5 10

<210> 17
<211> 13
<212> PRT
<213> homo sapiens

<400> 17

Gln Ser Leu Asp Gly Ser Arg Arg Ser Gly Tyr Ile Thr
1 5 10

<210> 18
<211> 13
<212> PRT
<213> homo sapiens

<400> 18

Pro Pro Glu Arg Tyr Thr Ser Arg Tyr Tyr Leu Lys Phe
1 5 10

<210> 19
<211> 18
<212> PRT
<213> homo sapiens

<400> 19

Phe Pro Glu Arg Ser Arg Leu Gln Arg Glu Ala Glu Tyr Phe Glu Leu
1 5 10 15

Pro Glu

<210> 20
<211> 14

<212> PRT
 <213> homo sapiens

<400> 20

Phe Gly Asp Thr Leu Asn Glu Ser Arg Asp Pro Asp Arg Pro
 1 5 10

<210> 21
 <211> 20
 <212> PRT
 <213> homo sapiens

<400> 21

Leu Ser Glu Ser Gly Phe His Met Val Ala Cys Ser Ser Thr Gly Thr
 1 5 10 15

Cys Ala Phe Ala
 20

<210> 12
 <211> 8
 <212> PRT
 <213> bacteriophage T7

<400> 12

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 23
 <211> 733
 <212> DNA
 <213> homo sapiens

<400> 23

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aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga	120
tctcccgga ccttgaggtc acatgcgtgg tgggtggacgt aagccaagaa gaccctgagg	180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg	240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact	300
ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccatcg	360
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc	420
cctcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct	480
atccaagcga cctgcctgtg gactgggaga gcaatgggca gccggagaac aactacaaga	540
ccacgcctcc cgtgctggac tccgacggct ccttcttctt ctacagcaag ctcaccgtgg	600

acaagagtag gtggcagag gggaaagtct tctcatgctc cgtgatgcac gaggcctctgc 660
 acaaccarta cagccagag agcctctccc tgtctccggg taaatgagtg cgaacggccgc 720
 gactctagag gat 733

<210> 24
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 24
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<210> 25
 <211> 37
 <212> DNA
 <213> Homo sapiens

<400> 25
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<210> 26
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 26
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<210> 27
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 <212> DNA
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<400> 27
 gcagcagtcg accttgctga aggcctgctc caggaag 37

<210> 28
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 28
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<210> 29
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 <212> DNA
 <213> Homo sapiens

<400> 29
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<210> 30
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<400> 30
 gaggtgcagc tggaggagtc tgg 23

<210> 31
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 <212> DNA
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35 40 45

Gln Glu Ser Lys Cys His Leu Ile Glu Thr Asn Ile Arg Asp Gln Glu
50 55 60

Glu Leu Lys Gly Lys Lys Val Pro Gln Tyr Pro Cys Leu Trp Val Asn
65 70 75 80

Val Ser Ala Ala Gly Arg Trp Ala Val Leu Tyr His Thr Glu Asp Thr
85 90 95

Arg Asp Gln Asn Gln Gln Cys Ser Tyr Ile Pro Gly Ser Val Asp Asn
100 105 110

Tyr Gln Thr Ala Arg Ala Asp Val Glu Lys Val Arg Ala Lys Phe Gln
115 120 125

Glu Gln Gln Val Phe Tyr Cys Phe Ser Ala Pro Arg Gly Asn Glu Thr

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Leu Phe Trp Pro Thr Phe Leu Leu Thr Gly Gly Leu Leu Ile Ile Ala		
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Thr Ile Gly Thr Leu Thr Lys Asn Asn Asp Thr Met Leu Ser Ala Met		
	35	40 45
Phe Ser Gly Arg Met Glu Val Leu Thr Asp Ser Glu Gly Trp Ile Leu		
	50	55 60
Ile Asp Arg Cys Gly Asn His Phe Gly Ile Ile Leu Asn Tyr Leu Arg		
65	70	75 80
Asp Gly Thr Val Pro Leu Pro Glu Thr Asn Lys Glu Ile Ala Glu Leu		
	85	90 95
Leu Ala Glu Ala Lys Tyr Tyr Cys Ile Thr Glu Leu Ala Ile Ser Cys		
	100	105 110
Glu Arg Ala Leu Tyr Ala His Gln Glu Pro Lys Pro Ile Cys Arg Ile		
	115	120 125
Pro Leu Ile Thr Ser Gln Lys Glu Glu Gln Leu Leu Leu Ser Val Ser		
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Leu Lys Pro Ala Val Ile Leu Val Val Gln Arg Gln Asn Asn Lys Tyr		
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Ser Tyr Thr Ser Thr Ser Asp Asp Asn Leu Leu Lys Asn Ile Glu Leu		
	165	170 175
Phe Asp Lys Leu Ser Leu Arg Phe Asn Glu Arg Ile Leu Phe Ile Lys		
	180	185 190
Asp Val Ile Gly Pro Ser Glu Ile Cys Cys Trp Ser Phe Tyr Gly His		
	195	200 205

Gly Lys Lys Val Ala Glu Val Cys Cys Thr Ser Ile Val Tyr Ala Thr
 210 215 220

Asp Arg Lys His Thr Lys Val Glu Phe Pro Glu Ala Arg Ile Tyr Glu
 225 230 235 240

Glu Thr Leu Gln Val Leu Leu Tyr Glu Asn Arg Asn Ala Pro Asp Gln
 245 250 255

Glu Leu Met Gln Ala Thr Ser Ser Ala Arg Val Gly Ser Ala Ser Gly
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